

Sub A

SEQUENCE LISTING

<110> ANTEXBIOLOGICS, INC.

<120> CHLAMYDIA PROTEIN, GENE SEQUENCE AND USES THEREOF

<130> 7969-076

<140>

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<150> 08/942,596

<151> 1997-10-02

<160> 41

<170> PatentIn Ver. 2.0

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:  
recombinant expression vector

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<212> PRT  
<213> Chlamydia

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35 40 45

Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe Ser Ala Gly Glu  
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Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala Leu Pro Leu Ser  
65 70 75 80

Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu Gly Arg Gly His  
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Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn Gly Ala Ala Leu  
100 105 110

Ser Asn Ser Ala Ala Asp Gly Leu Phe Thr Ile Glu Gly Phe Lys Glu  
115 120 125

Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu Ala Val Leu Pro Ala Ala  
130 135 140

Thr Thr Asn Lys Gly Ser Gln Thr Pro Thr Thr Ser Thr Pro Ser  
145 150 155 160

Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu Asn Asn Glu  
165 170 175

Lys Phe Ser Phe Tyr Ser Asn Leu Val Ser Gly Asp Gly Gly Ala Ile  
180 185 190

Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys Leu Cys Val Phe  
195 200 205

Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys Gln Val Val Thr  
210 215 220

Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala Phe Val Ala Asn  
225 230 235 240

Val Ala Gly Val Arg Gly Gly Ile Ala Ala Val Gln Asp Gly Gln  
245 250 255

Gln Gly Val Ser Ser Ser Thr Ser Thr Glu Asp Pro Val Val Ser Phe  
260 265 270

Ser Arg Asn Thr Ala Val Glu Phe Asp Gly Asn Val Ala Arg Val Gly  
275 280 285

Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala Phe Leu Asn Asn Gly Lys  
290 295 300

Thr Leu Phe Leu Asn Asn Val Ala Ser Pro Val Tyr Ile Ala Ala Lys  
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Gln Pro Thr Ser Gly Gln Ala Ser Asn Thr Ser Asn Asn Tyr Gly Asp  
325 330 335

Gly Gly Ala Ile Phe Cys Lys Asn Gly Ala Gln Ala Gly Ser Asn Asn  
340 345 350

Ser Gly Ser Val Ser Phe Asp Gly Glu Gly Val Val Phe Phe Ser Ser  
355 360 365

Asn Val Ala Ala Gly Lys Gly Ala Ile Tyr Ala Lys Lys Leu Ser  
370 375 380

Val Ala Asn Cys Gly Pro Val Gln Phe Leu Arg Asn Ile Ala Asn Asp  
385 390 395 400

Gly Gly Ala Ile Tyr Leu Gly Glu Ser Gly Glu Leu Ser Leu Ser Ala  
405 410 415

Asp Tyr Gly Asp Ile Ile Phe Asp Gly Asn Leu Lys Arg Thr Ala Lys  
420 425 430

Glu Asn Ala Ala Asp Val Asn Gly Val Thr Val Ser Ser Gln Ala Ile  
435 440 445

Ser Met Gly Ser Gly Gly Lys Ile Thr Thr Leu Arg Ala Lys Ala Gly  
450 455 460

His Gln Ile Leu Phe Asn Asp Pro Ile Glu Met Ala Asn Gly Asn Asn  
465 470 475 480

Gln Pro Ala Gln Ser Ser Lys Leu Leu Lys Ile Asn Asp Gly Glu Gly  
485 490 495

Tyr Thr Gly Asp Ile Val Phe Ala Asn Gly Ser Ser Thr Leu Tyr Gln  
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Asn Val Thr Ile Glu Gln Gly Arg Ile Val Leu Arg Glu Lys Ala Lys  
515 520 525

Leu Ser Val Asn Ser Leu Ser Gln Thr Gly Gly Ser Leu Tyr Met Glu  
530 535 540

Ala Gly Ser Thr Trp Asp Phe Val Thr Pro Gln Pro Pro Gln Gln Pro  
545 550 555 560

Pro Ala Ala Asn Gln Leu Ile Thr Leu Ser Asn Leu His Leu Ser Leu  
565 570 575

Ser Ser Leu Leu Ala Asn Asn Ala Val Thr Asn Pro Pro Thr Asn Pro  
580 585 590

Pro Ala Gln Asp Ser His Pro Ala Val Ile Gly Ser Thr Thr Ala Gly  
595 600 605

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610 615 620

Ala Tyr Asp Arg Tyr Asp Trp Leu Gly Ser Asn Gln Lys Ile Asn Val  
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Lys Ala Thr Trp Thr Lys Thr Gly Tyr Asn Pro Gly Pro Glu Arg Val  
690 695 700

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725 730 735

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740 745 750

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755 760 765

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Glu Val Phe Gly Arg Ser Lys Asp Tyr Val Val Cys Arg Ser Asn His  
785 790 795 800

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820 825 830

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Val Arg Trp Asp Asn Asn Cys Leu Ala Gly Glu Ile Gly Ala Gly Leu  
850 855 860

Pro Ile Val Ile Thr Pro Ser Lys Leu Tyr Leu Asn Glu Leu Arg Pro  
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Phe Val Gln Ala Glu Phe Ser Tyr Ala Asp His Glu Ser Phe Thr Glu  
885 890 895

Glu Gly Asp Gln Ala Arg Ala Phe Lys Ser Gly His Leu Leu Asn Leu  
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Ser Val Pro Val Gly Val Lys Phe Asp Arg Cys Ser Ser Thr His Pro  
915 920 925

Asn Lys Tyr Ser Phe Met Ala Ala Tyr Ile Cys Asp Ala Tyr Arg Thr  
930 935 940

Ile Ser Gly Thr Glu Thr Thr Leu Leu Ser His Gln Glu Thr Trp Thr  
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Thr Asp Ala Phe His Leu Ala Arg His Gly Val Val Val Arg Gly Ser  
965 970 975

Met Tyr Ala Ser Leu Thr Ser Asn Ile Glu Val Tyr Gly His Gly Arg  
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Arg Val Arg Phe  
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<213> Chlamydia

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35 40 45

Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe Ser Ala Gly Glu  
50 55 60

Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala Leu Pro Leu Ser  
65 70 75 80

Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu Gly Arg Gly His  
85 90 95

Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn Gly Ala Ala Leu  
100 105 110

Ser Asp Ser Ala Asn Ser Gly Leu Phe Thr Ile Glu Gly Phe Lys Glu

115 120 125  
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165 170 175  
Lys Phe Ser Phe Tyr Ser Asn Ser Val Ser Gly Asp Gly Gly Ala Ile  
180 185 190  
Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys Leu Cys Val Phe  
195 200 205  
Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys Gln Val Val Thr  
210 215 220  
Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala Phe Val Ala Asn  
225 230 235 240  
Val Ala Gly Val Arg Gly Gly Ile Ala Ala Val Gln Asp Gly Gln  
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Gln Gly Val Ser Ser Ser Thr Ser Thr Glu Asp Pro Val Val Ser Phe  
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Ser Arg Asn Thr Ala Val Glu Phe Asp Gly Asn Val Ala Arg Val Gly  
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Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala Phe Leu Asn Asn Gly Lys  
290 295 300  
Thr Leu Phe Leu Asn Asn Val Ala Ser Pro Val Tyr Ile Ala Ala Glu  
305 310 315 320  
Gln Pro Thr Asn Gly Gln Ala Ser Asn Thr Ser Asp Asn Tyr Gly Asp  
325 330 335  
Gly Gly Ala Ile Phe Cys Lys Asn Gly Ala Gln Ala Ala Gly Ser Asn  
340 345 350  
Asn Ser Gly Ser Val Ser Phe Asp Gly Glu Gly Val Val Phe Phe Ser  
355 360 365  
Ser Asn Val Ala Ala Gly Lys Gly Ala Ile Tyr Ala Lys Lys Leu

370	375	380
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385	390	395
Asp Gly Gly Ala Ile Tyr Leu Gly Glu Ser Gly Glu Leu Ser Leu Ser		
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Ala Asp Tyr Gly Asp Met Ile Phe Asp Gly Asn Leu Lys Arg Thr Ala		
420	425	430
Lys Glu Asn Ala Ala Asp Val Asn Gly Val Thr Val Ser Ser Gln Ala		
435	440	445
Ile Ser Met Gly Ser Gly Gly Lys Ile Thr Thr Leu Arg Ala Lys Ala		
450	455	460
Gly His Gln Ile Leu Phe Asn Asp Pro Ile Glu Met Ala Asn Gly Asn		
465	470	475
480		
Asn Gln Pro Ala Gln Ser Ser Glu Pro Leu Lys Ile Asn Asp Gly Glu		
485	490	495
Gly Tyr Thr Gly Asp Ile Val Phe Ala Asn Gly Asn Ser Thr Leu Tyr		
500	505	510
Gln Asn Val Thr Ile Glu Gln Gly Arg Ile Val Leu Arg Glu Lys Ala		
515	520	525
Lys Leu Ser Val Asn Ser Leu Ser Gln Thr Gly Ser Leu Tyr Met		
530	535	540
Glu Ala Gly Ser Thr Leu Asp Phe Val Thr Pro Gln Pro Pro Gln Gln		
545	550	555
560		
Pro Pro Ala Ala Asn Gln Ser Ile Thr Leu Ser Asn Leu His Leu Ser		
565	570	575
Leu Ser Ser Leu Leu Ala Asn Asn Ala Val Thr Asn Pro Pro Thr Asn		
580	585	590
Pro Pro Ala Gln Asp Ser His Pro Ala Val Ile Gly Ser Thr Thr Ala		
595	600	605
Gly Ser Val Thr Ile Ser Gly Pro Ile Phe Phe Glu Asp Leu Asp Asp		
610	615	620
Thr Ala Tyr Asp Arg Tyr Asp Trp Leu Gly Ser Asn Gln Lys Ile Asp		

625                    630                    635                    640

Val Leu Lys Leu Gln Leu Gly Thr Gln Pro Pro Ala Asn Ala Pro Ser  
                   645                    650                    655

Asp Leu Thr Leu Gly Asn Glu Met Pro Lys Tyr Gly Tyr Gln Gly Ser  
                   660                    665                    670

Trp Lys Leu Ala Trp Asp Pro Asn Thr Ala Asn Asn Gly Pro Tyr Thr  
                   675                    680                    685

Leu Lys Ala Thr Trp Thr Lys Thr Gly Tyr Asn Pro Gly Pro Glu Arg  
                   690                    695                    700

Val Ala Ser Leu Val Pro Asn Ser Leu Trp Gly Ser Ile Leu Asp Ile  
                   705                    710                    715                    720

Arg Ser Ala His Ser Ala Ile Gln Ala Ser Val Asp Gly Arg Ser Tyr  
                   725                    730                    735

Cys Arg Gly Leu Trp Val Ser Gly Val Ser Asn Phe Phe Tyr His Asp  
                   740                    745                    750

Arg Asp Ala Leu Gly Gln Gly Tyr Arg Tyr Ile Ser Gly Gly Tyr Ser  
                   755                    760                    765

Leu Gly Ala Asn Ser Tyr Phe Gly Ser Ser Met Phe Gly Leu Ala Phe  
                   770                    775                    780

Thr Glu Val Phe Gly Arg Ser Lys Asp Tyr Val Val Cys Arg Ser Asn  
                   785                    790                    795                    800

His His Ala Cys Ile Gly Ser Val Tyr Leu Ser Thr Lys Gln Ala Leu  
                   805                    810                    815

Cys Gly Ser Tyr Val Phe Gly Asp Ala Phe Ile Arg Ala Ser Tyr Gly  
                   820                    825                    830

Phe Gly Asn Gln His Met Lys Thr Ser Tyr Thr Phe Ala Glu Glu Ser  
                   835                    840                    845

Asp Val Cys Trp Asp Asn Asn Cys Leu Val Gly Glu Ile Gly Val Gly  
                   850                    855                    860

Leu Pro Ile Val Ile Thr Pro Ser Lys Leu Tyr Leu Asn Glu Leu Arg  
                   865                    870                    875                    880

Pro Phe Val Gln Ala Glu Phe Ser Tyr Ala Asp His Glu Ser Phe Thr

885

890

895

Glu Glu Gly Asp Gln Ala Arg Ala Phe Arg Ser Gly His Leu Met Asn  
900 905 910

Leu Ser Val Pro Val Gly Val Lys Phe Asp Arg Cys Ser Ser Thr His  
915 920 925

Pro Asn Lys Tyr Ser Phe Met Gly Ala Tyr Ile Cys Asp Ala Tyr Arg  
930 935 940

Thr Ile Ser Gly Thr Gln Thr Thr Leu Leu Ser His Gln Glu Thr Trp  
945 950 955 960

Thr Thr Asp Ala Phe His Leu Ala Arg His Gly Val Ile Val Arg Gly  
965 970 975

Ser Met Tyr Ala Ser Leu Thr Ser Asn Ile Glu Val Tyr Gly His Gly  
980 985 990

Arg Tyr Glu Tyr Arg Asp Thr Ser Arg Gly Tyr Gly Leu Ser Ala Gly  
995 1000 1005

Ser Lys Val Arg Phe  
1010

<210> 16

<211> 1013

<212> PRT

<213> Chlamydia

<400> 16

Met Gln Thr Ser Phe His Lys Phe Phe Leu Ser Met Ile Leu Ala Tyr  
1 5 10 15

Ser Cys Cys Ser Leu Thr Gly Gly Tyr Ala Ala Glu Ile Met Val  
20 25 30

Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu Thr Val Ser Phe Pro Tyr  
35 40 45

Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe Ser Ala Gly Glu  
50 55 60

Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala Leu Pro Leu Ser  
65 70 75 80

Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu Gly Arg Gly His  
 85 90 95

Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn Gly Ala Ala Leu  
 100 105 110

Ser Asp Ser Ala Asn Ser Gly Leu Phe Thr Ile Glu Gly Phe Lys Glu  
 115 120 125

Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu Ala Val Leu Pro Ala Ala  
 130 135 140

Thr Thr Asn Asn Gly Ser Gln Thr Pro Thr Thr Ser Thr Pro Ser  
 145 150 155 160

Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu Asn Asn Glu  
 165 170 175

Lys Phe Ser Phe Tyr Ser Asn Leu Val Ser Gly Asp Gly Gly Thr Ile  
 180 185 190

Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys Leu Cys Val Phe  
 195 200 205

Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys Gln Val Val Thr  
 210 215 220

Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala Phe Ile Ala Asn  
 225 230 235 240

Val Ala Gly Val Arg Gly Gly Ile Ala Ala Val Gln Asp Gly Gln  
 245 250 255

Gln Gly Val Ser Ser Ser Thr Ser Thr Glu Asp Pro Val Val Ser Phe  
 260 265 270

Ser Arg Asn Thr Ala Val Glu Phe Asp Gly Asn Val Ala Arg Val Gly  
 275 280 285

Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala Phe Leu Asn Asn Gly Lys  
 290 295 300

Thr Leu Phe Leu Asn Asn Val Ala Ser Pro Val Tyr Ile Ala Ala Glu  
 305 310 315 320

Gln Pro Thr Asn Gly Gln Ala Ser Asn Thr Ser Asp Asn Tyr Gly Asp  
 325 330 335

Gly Gly Ala Ile Phe Cys Lys Asn Gly Ala Gln Ala Ala Gly Ser Asn  
340 345 350

Asn Ser Gly Ser Val Ser Phe Asp Gly Glu Gly Val Val Phe Phe Ser  
355 360 365

Ser Asn Val Ala Ala Gly Lys Gly Gly Ala Ile Tyr Ala Lys Lys Leu  
370 375 380

Ser Val Ala Asn Cys Gly Pro Val Gln Phe Leu Gly Asn Ile Ala Asn  
385 390 395 400

Asp Gly Gly Ala Ile Tyr Leu Gly Glu Ser Gly Glu Leu Ser Leu Ser  
405 410 415

Ala Asp Tyr Gly Asp Ile Ile Phe Asp Gly Asn Leu Lys Arg Thr Ala  
420 425 430

Lys Glu Asn Ala Ala Asp Val Asn Gly Val Thr Val Ser Ser Gln Ala  
435 440 445

Ile Ser Met Gly Ser Gly Gly Lys Ile Thr Thr Leu Arg Ala Lys Ala  
450 455 460

Gly His Gln Ile Leu Phe Asn Asp Pro Ile Glu Met Ala Asn Gly Asn  
465 470 475 480

Asn Gln Pro Ala Gln Ser Ser Glu Pro Leu Lys Ile Asn Asp Gly Glu  
485 490 495

Gly Tyr Thr Gly Asp Ile Val Phe Ala Asn Gly Asn Ser Thr Leu Tyr  
500 505 510

Gln Asn Val Thr Ile Glu Gln Gly Arg Ile Val Leu Arg Glu Lys Ala  
515 520 525

Lys Leu Ser Val Asn Ser Leu Ser Gln Thr Gly Gly Ser Leu Tyr Met  
530 535 540

Glu Ala Gly Ser Thr Leu Asp Phe Val Thr Pro Gln Pro Pro Gln Gln  
545 550 555 560

Pro Pro Ala Ala Asn Gln Leu Ile Thr Leu Ser Asn Leu His Leu Ser  
565 570 575

Leu Ser Ser Leu Leu Ala Asn Asn Ala Val Thr Asn Pro Pro Thr Asn  
580 585 590

Pro Pro Ala Gln Asp Ser His Pro Ala Val Ile Gly Ser Thr Thr Ala  
595 600 605

Gly Pro Val Thr Ile Ser Gly Pro Phe Phe Phe Glu Asp Leu Asp Asp  
610 615 620

Thr Ala Tyr Asp Arg Tyr Asp Trp Leu Gly Ser Asn Gln Lys Ile Asp  
625 630 635 640

Val Leu Lys Leu Gln Leu Gly Thr Gln Pro Ser Ala Asn Ala Pro Ser  
645 650 655

Asp Leu Thr Leu Gly Asn Glu Met Pro Lys Tyr Gly Tyr Gln Gly Ser  
660 665 670

Trp Lys Leu Ala Trp Asp Pro Asn Thr Ala Asn Asn Gly Pro Tyr Thr  
675 680 685

Leu Lys Ala Thr Trp Thr Lys Thr Gly Tyr Asn Pro Gly Pro Glu Arg  
690 695 700

Val Ala Ser Leu Val Pro Asn Ser Leu Trp Gly Ser Ile Leu Asp Ile  
705 710 715 720

Arg Ser Ala His Ser Ala Ile Gln Ala Ser Val Asp Gly Arg Ser Tyr  
725 730 735

Cys Arg Gly Leu Trp Val Ser Gly Val Ser Asn Phe Ser Tyr His Asp  
740 745 750

Arg Asp Ala Leu Gly Gln Gly Tyr Arg Tyr Ile Ser Gly Gly Tyr Ser  
755 760 765

Leu Gly Ala Asn Ser Tyr Phe Gly Ser Ser Met Phe Gly Leu Ala Phe  
770 775 780

Thr Glu Val Phe Gly Arg Ser Lys Asp Tyr Val Val Cys Arg Ser Asn  
785 790 795 800

His His Ala Cys Ile Gly Ser Val Tyr Leu Ser Thr Lys Gln Ala Leu  
805 810 815

Cys Gly Ser Tyr Leu Phe Gly Asp Ala Phe Ile Arg Ala Ser Tyr Gly  
820 825 830

Phe Gly Asn Gln His Met Lys Thr Ser Tyr Thr Phe Ala Glu Glu Ser  
835 840 845

Asp Val Arg Trp Asp Asn Asn Cys Leu Val Gly Glu Ile Gly Val Gly  
850 855 860

Leu Pro Ile Val Thr Thr Pro Ser Lys Leu Tyr Leu Asn Glu Leu Arg  
865 870 875 880

Pro Phe Val Gln Ala Glu Phe Ser Tyr Ala Asp His Glu Ser Phe Thr  
885 890 895

Glu Glu Gly Asp Gln Ala Arg Ala Phe Arg Ser Gly His Leu Met Asn  
900 905 910

Leu Ser Val Pro Val Gly Val Lys Phe Asp Arg Ser Cys Ser Thr His  
915 920 925

Pro Asn Lys Tyr Ser Phe Met Gly Ala Tyr Ile Cys Asp Ala Tyr Arg  
930 935 940

Thr Ile Ser Gly Thr Gln Thr Leu Leu Ser His Gln Glu Thr Trp  
945 950 955 960

Thr Thr Asp Ala Phe His Leu Ala Arg His Gly Val Ile Val Arg Gly  
965 970 975

Ser Met Tyr Ala Ser Leu Thr Ser Asn Ile Glu Val Tyr Gly His Gly  
980 985 990

Arg Tyr Glu Tyr Arg Asp Thr Ser Arg Gly Tyr Gly Leu Ser Ala Gly  
995 1000 1005

Ser Lys Val Arg Phe  
1010

<210> 17

<211> 505

<212> PRT

<213> Chlamydia

<400> 17

Glu Ile Met Val Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu Thr Val  
1 5 10 15

Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe  
20 25 30

Ser Ala Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala  
35 40 45

Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu  
50 55 60

Gly Arg Gly His Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn  
65 70 75 80

Gly Ala Ala Leu Ser Asn Ser Ala Ala Asp Gly Leu Phe Thr Ile Glu  
85 90 95

Gly Phe Lys Glu Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu Ala Val  
100 105 110

Leu Pro Ala Ala Thr Thr Asn Lys Gly Ser Gln Thr Pro Thr Thr Thr  
115 120 125

Ser Thr Pro Ser Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu  
130 135 140

Leu Asn Asn Glu Lys Phe Ser Phe Tyr Ser Asn Leu Val Ser Gly Asp  
145 150 155 160

Gly Gly Ala Ile Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys  
165 170 175

Leu Cys Val Phe Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys  
180 185 190

Gln Val Val Thr Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala  
195 200 205

Phe Val Ala Asn Val Ala Gly Val Arg Gly Gly Ile Ala Ala Val  
210 215 220

Gln Asp Gly Gln Gln Gly Val Ser Ser Ser Thr Ser Thr Glu Asp Pro  
225 230 235 240

Val Val Ser Phe Ser Arg Asn Thr Ala Val Glu Phe Asp Gly Asn Val  
245 250 255

Ala Arg Val Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala Phe Leu  
260 265 270

Asn Asn Gly Lys Thr Leu Phe Leu Asn Asn Val Ala Ser Pro Val Tyr  
275 280 285

Ile Ala Ala Lys Gln Pro Thr Ser Gly Gln Ala Ser Asn Thr Ser Asn  
290 295 300

Asn Tyr Gly Asp Gly Gly Ala Ile Phe Cys Lys Asn Gly Ala Gln Ala  
305 310 315 320

Gly Ser Asn Asn Ser Gly Ser Val Ser Phe Asp Gly Glu Gly Val Val  
325 330 335

Phe Phe Ser Ser Asn Val Ala Ala Gly Lys Gly Gly Ala Ile Tyr Ala  
340 345 350

Lys Lys Leu Ser Val Ala Asn Cys Gly Pro Val Gln Phe Leu Arg Asn  
355 360 365

Ile Ala Asn Asp Gly Gly Ala Ile Tyr Leu Gly Glu Ser Gly Glu Leu  
370 375 380

Ser Leu Ser Ala Asp Tyr Gly Asp Ile Ile Phe Asp Gly Asn Leu Lys  
385 390 395 400

Arg Thr Ala Lys Glu Asn Ala Ala Asp Val Asn Gly Val Thr Val Ser  
405 410 415

Ser Gln Ala Ile Ser Met Gly Ser Gly Gly Lys Ile Thr Thr Leu Arg  
420 425 430

Ala Lys Ala Gly His Gln Ile Leu Phe Asn Asp Pro Ile Glu Met Ala  
435 440 445

Asn Gly Asn Asn Gln Pro Ala Gln Ser Ser Lys Leu Leu Lys Ile Asn  
450 455 460

Asp Gly Glu Gly Tyr Thr Gly Asp Ile Val Phe Ala Asn Gly Ser Ser  
465 470 475 480

Thr Leu Tyr Gln Asn Val Thr Ile Glu Gln Gly Arg Ile Val Leu Arg  
485 490 495

Glu Lys Ala Lys Leu Ser Val Asp Ser  
500 505

<210> 18

<211> 57

<212> DNA

<213> Chlamydia

<400> 18

aaggcccaa ttacgcagag ctcgagagaa attatggttc ctcaaggaat ttacgat 57

<210> 19  
<211> 20  
<212> DNA  
<213> Chlamydia

<400> 19  
cgctctagaa ctagtggatc

20

<210> 20  
<211> 22  
<212> DNA  
<213> Chlamydia

<400> 20  
atggttcctc aaggaattta cg

22

<210> 21  
<211> 19  
<212> DNA  
<213> Chlamydia

<400> 21  
ggtcccccat cagcgggag

19

<210> 22  
<211> 1515  
<212> DNA  
<213> Chlamydia

<400> 22  
gaaatcatgg ttcctcaagg aatttacgat ggggagacgt taactgtatc atttccctat 60  
actgttatacg gagatccgag tgggactact gtttttctg caggagagtt aacattaaaa 120  
aatcttgaca attctattgc agcttgccct ttaagttgtt ttggaaactt attaggagtt 180  
tttactgttt tagggagagg acactcggtt actttcgaga acatacggac ttctacaaat 240  
ggggcagctc taagtaatacg cgctgctgat ggactgttta ctattgaggg ttttaaagaa 300  
ttatcctttt ccaattgcaa ttcatctactt gccgtactgc ctgctgcaac gactaataag 360  
ggtagccaga ctccgacgac aacatctaca ccgtctaattt gtactattta ttctaaaaca 420  
gatctttgt tactcaataa tgagaagttc tcattctata gtaattttgt ctctggagat 480  
gggggagcta tagatgctaa gagcttaacg gttcaaggaa ttagcaagct ttgtgtcttc 540  
caagaaaaata ctgctcaagc tgatggggaa gttgtcaag tagtcaccag ttctctgtct 600  
atggcttaacg aggctcctat tgcctttgtc gcgaatgtt caggagtaag agggggaggg 660  
attgctgctg ttcatggatgg gcagcaggaa gtgtcatcat ctacttcaac agaagatcca 720  
gtagtaagtt ttccagaaa tactgcggta gagttgtatc ggaacgttagc ccgagtagga 780  
ggagggattt actcctacgg gaacgttgct ttcctgaata atgaaaaac cttgtttctc 840  
aacaatgttgc ttctccctgt ttacattgtc gctaagcaac caacaagtgg acaggcttct 900  
aatacggatc ataattacgg agatggagga gctatctt gtaagaatgg tgcgcaagca 960  
ggatccaata actctggatc agttccctt gatggagagg gagtagttt cttagtagc 1020

aatgttagctg ctgggaaagg gggagctatt tatgc当地 1080  
ggccctgtac aatttttaag gaatatcgct aatgatgggt gaggcattta ttttaggagaa 1140  
tctggagagc tcagtttac tgctgattat ggagatatta ttttcgatgg gaatcttaaa 1200  
agaacagcca aagagaatgc tgccgatgtt aatggcgtaa ctgtgtcctc acaagccatt 1260  
tcgatggat cgggagggaa aataacgaca ttaagagcta aagcagggca tcagattctc 1320  
ttaatgatc ccatcgagat ggcaaacgga aataaccagc cagcgcagtc ttccaaactt 1380  
ctaaaaatta acgatggtga aggatacaca ggggatattt ttttgctaa tggaaaggcagt 1440  
actttgtacc aaaatgttac gatagagcaa ggaaggattt ttcttcgtga aaaggcaaaa 1500  
ttatcagtga attct 1515

<210> 23

<211> 3354

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

recombinant expression vector

<400> 23

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ttaaatgggg ggggttatgc agaaatcatg gttcctcaag gaatttacga tggggagacg 120  
ttaactgtat cattcccta tactttata ggagatccga gtggactac tggggacttct 180  
gcaggaggt taacgttaaa aaatcttgac aattcttattt cagcttgcctttaagggtt 240  
tttgggaact tattaggag ttttactgtt ttagggagag gacactcggtt gactttcgag 300  
aacatacggc cttctacaaa tggagctgca ctaagtgaca gcgctaatacg cgggttattt 360  
actattgagg gttttaaaga attatctttt tccaaattgca acccattact tgccgtactg 420  
cctgctgcaa cgactaataa tggtagccag actccgtcga caacatctac accgtctaat 480  
ggtactattt attctaaaac agatctttt ttaactcaata atgagaagtt ctcattctat 540  
agtaattcag tctctggaga tggggagct atagatgcta agagcttaac ggttcaagga 600  
attagcaagc tttgtgtctt ccaagaaaat actgctcaag ctgatgggg agcttgc当地 660  
gtagtcacca gttctctgc tatggtaac gaggctccta ttgccttgc agcgaatgtt 720  
gcaggagtaa gagggggagg gattgctgct gttcaggatg ggcagcaggag tgggttgc当地 780  
tctacttcaa cagaagatcc agtagtaagt tttccagaa atactgcggg agagtttgc当地 840  
gggaaacgttag cccgagtagg aggagggatt tactcttacg ggaacgttgc ttctgtat 900  
aatggaaaaa cttgtttctt caacaatgtt gcttctccctt tttacattgc tgctgagcaa 960  
ccaacaaatg gacaggcttc taatacgagt gataattacg gagatggagg agctatctc 1020  
tgtaagaatg gtgc当地 agcaggatcc aataactctg gatcaggatcc ctttgc当地 1080  
gaggagtag ttttctttag tagcaatgtt gctgctggaa aagggggagc tattttatgc当地 1140  
aaaaagctct cgggttgc当地 ctgtggccct gtacaactct tagggatata cgctaatgtt 1200  
ggggagcga tttatggat agaattctggaa gagctcaggat tattctgttgc ttatggagat 1260  
atgattttcg atggaaatct taaaagaaca gccaagaga atgctgccga tggaaatggc 1320  
gtaaactgtgt cctcacaagc catttcgatg ggatcggggag ggaaaataac gacattaaga 1380  
gctaaagcag ggc当地 agatggc当地 agatggc当地 cggaaaataac 1440  
cagccagcgc agtctccga acctctaaaa attaacgatg gtgaaggata cacagggat 1500  
attgttttgc当地 ctaatggaaa cagtagtttacccaaatg ttacgataga gcaagggagg 1560  
attgttcttc当地 gtggaaaaggc aaaattatca gtgaattctc taagtcagac aggtggagat 1620  
ctgtatatgg aagctggag tacattggat tttgtactc cacaaccacc acaacagcct 1680

cctggcgcta atcagtcgat cacgcttcc aatctgcatt tgtctcttc ttctttgtta 1740  
gcaaacaatg cagttacgaa tcctcctacc aatcctccag cgcaagattc tcatcctgca 1800  
gtcattggta gcacaactgc tggttctgtt acaattagtg ggctatctt tttgaggat 1860  
ttggatgata cagcttatga taggtatgat tggctaggtt ctaatcaaaa aatcgatgtc 1920  
ctgaaattac agttagggac tcagccccca gctaattcccc catcagattt gactctaggg 1980  
aatgagatgc ctaagtatgg ctatcaagga agctggaagc ttgcgtggta tcctaataca 2040  
gcaaataatg gtccttatac tctgaaaagct acatggacta aaactggta taatcctggg 2100  
cctgagcgag tagcttctt ggttccaaat agttatgg gatccatctt agatatacga 2160  
tctgcgcatt cagcaattca agcaagtgtg gatggcgct cttattgtcg aggattatgg 2220  
gttctggag tttcgaattt cttctatcat gaccgcgtat ctttaggtca gggatatcg 2280  
tatattagtg ggggttattc cttaggagca aactcctact ttggatcatc gatgttgg 2340  
ctagcattt ctgaagtatt tggtagatct aaagattatg tagtgtgtcg ttccaatcat 2400  
catgctgca taggatccgt ttatctatct accaaacagg ctttatgtgg atcttatgtg 2460  
tttggagatg cgtttattcg tgctagctac gggtttggta atcagcatat gaaaacctca 2520  
tatacattt cagaggagag cgatgttgt tggataata actgtctggt tggagagatt 2580  
ggagtggat taccgattgt gattactcca tctaagctt atttgaatga gttgcgtcct 2640  
ttcgtgcaag ctgagtttc ttatgccat catgaatctt ttacagagga aggcgatcaa 2700  
gctcggcat tcaggagtgg acatctcatg aatctatcag ttccctgttgg agtaaaaattt 2760  
gategatgtt cttagtacaca ccctaataaa tatagcttta tggggctta tatctgtat 2820  
gcttatcgca ccatctctgg gactcagaca acactcctat cccatcaaga gacatggaca 2880  
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ctaacaagca atatagaagt atatggccat ggaagatatg agtacgcaga tacttctcg 3000  
ggttatggtt tgagtgcagg aagtaaagtc cggttctaaa aatattggtt agatagttaa 3060  
gtgttagcga tgccttttc tttgagatct acatcatttt gtttttagc ttgtttgtgt 3120  
tcctattcgt atggattcgc gagctctctt caagtgttta cacctaattt aaccactcct 3180  
ttaaggggg acgatgttta cttgaatgg aactgcgtt ttgtcaatgt ctatgcagg 3240  
gcagagaacg gctcaattat ctcaagctat ggcgacaatt taacgattac cggacaaaac 3300  
catacattat catttacaca ttctcaaggg ccagttcttc aaaattagcc ttca 3354

<210> 24

<211> 3324

<212> DNA

### <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
recombinant expression vector

<400> 24

atgcaaaacgt ctttccataa gttctttctt tcaatgatc tagcttattc ttgctgtct 60  
ttaagtgggg ggggttatgc agcagaatc atgattcctc aaggaattta cgatggggag 120  
acgttaactg tatcatttcc ctatactgtt ataggagatc cgagtgggac tactgtttt 180  
tctgcaggag agttaacgtt aaaaaatctt gacaattcta ttgcagctt gccttaagt 240  
tgaaaaatcc acattattagg gagttttact gttttaggga gaggacactc gttgacttcc 300  
gagaacatac ggacttctac aaatggagct gcactaagtg acagcgctaa tagcgggtta 360  
tttactattg agggttttaa agaattatct ttttccaatt gcaactcatt acttgcgtt 420  
ctgcctgctg caacgactaa taatggtagc cagactccga cgacaacatc tacaccgtct 480  
aatggtacta ttattctaa aacagatctt ttgttactca ataatgagaa gttctcattc 540

tatagttaatt tagtctctgg agatggggga actatacatg ctaagagctt aacgggttcaa 600  
ggaatttagca agctttgtgt cttccaaagaa aataactgctc aagctgatgg gggagcttgc 660  
caagtagtca ccagtttctc tgctatggct aacgaggctc ctattgcctt tatacgcaat 720  
gttgcaggag taagaggggg agggattgct gctgttcagg atggcagca gggagtgtca 780  
tcatctactt caacagaaga tccagtagta agttttcca gaaatactgc ggttagatgttt 840  
gatgggaacg tagcccgagt aggaggaggg atttactcct acggaaacgt tgctttcctg 900  
aataatggaa aaacccctgtt tctcaacaat gttgttctc ctgttacat tgctgctgag 960  
caaccaacaa atggacaggc ttctaaatacg agtataattt acggagatgg agagactatc 1020  
ttctgttaaga atgggtgcgc agcagcagga tccaataact ctggatcagt ttcccttgat 1080  
ggagagggag tagttttctt tagtagcaat gtagctgtg ggaaaggggg agctattat 1140  
gccaaaaaagc tctcggttgc taactgtggc cctgtacaat tcttagggaa tatcgctaat 1200  
gatgggtggag cgatttattt aggagaatct ggagagctca gtttatctgc tgattatgg 1260  
gatattattt tcgatggaa tcttaaaaga acagccaaag agaatgctgc cgatgttaat 1320  
ggcgtaactg tgcctcaca agccatttcg atgggatcgg gaggaaaat aacgacatta 1380  
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aaccagccag cgcaacttc cgaaccccta aaaattaacg atggtaagg atacacaggg 1500  
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<213> Chlamydia

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Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala Pro Leu  
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Ser Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu Gly Arg Gly  
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His Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn Gly Ala Ala  
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Leu

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<212> PRT

<213> Chlamydia

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Ser Leu Leu Ala Asn Asn Ala Val

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<210> 28

<211> 7

<212> PRT

<213> Chlamydia

<400> 28

Tyr Gly Asp Ile Ile Phe Asp  
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<211> 63

<212> PRT

<213> *Chlamydera cerviniventris*

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Thr Leu Thr Val Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly  
                   . 20                   25                   30

Thr Thr Val Phe Ser Ala Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn  
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Ser Ile Ala Ala Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu Gly  
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<212> PRT

<213> Chlamydia

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Ile Asn Asp Gly Glu Gly  
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<211> 14

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<213> Chlamydia

<400> 31

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Gly Ser Asn Gln Lys Ile Asn Val Leu Lys Leu Gln Leu  
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Gly Ser Asn Gln Lys Ile Asn Val Leu Lys Leu Gln Leu Gly Thr Lys  
35 40 45

Pro Pro Ala Asn Ala Pro Ser Asp Leu Thr Leu Gly Asn Glu Met Pro  
50 55 60

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Ala Pro Ile Ala Phe Val Ala Asn Val Ala Gly Val Arg Gly Gly Gly  
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Ile Ala Ala Val Gln Asp Gly Gln Gln Gly Val Ser Ser Ser Thr Ser  
35 40 45

Thr Glu Asp Pro Val Val Ser Phe Ser Arg Asn Thr Ala Val Glu Phe  
 50 55 60

Asp Gly Asn Val Ala Arg Val Gly Gly Gly Ile Tyr Ser Tyr Gly Asn  
65 70 75 80

Val Ala Phe Leu Asn Asn Gly Lys Thr Leu Phe Leu Asn Asn Val Ala  
85 90 95

Ser Pro Val Tyr Ile Ala Ala Lys Gln Pro Thr Ser Gly Gln Ala Ser  
100 105 110

Asn Thr Ser Asn Asn Tyr Gly Asp Gly Gly Ala Ile Phe Cys Lys Asn  
115 120 125

Gly Ala Gln Ala Gly Ser Asn Asn Ser Gly Ser Val Ser Phe Asp Gly  
130 135 140

Glu Gly Val Val Phe Phe Ser Ser Asn Val Ala Ala Gly Lys Gly Gly  
145 150 155 160

Ala Ile Tyr Ala Lys Lys Leu Ser Val Ala Asn Cys Gly Pro Val Gln

165 170 175

Phe Leu Arg Asn Ile Ala Asn Asp Gly Gly Ala Ile Tyr Leu Gly Glu  
180 185 190

Ser Gly Glu Leu Ser Leu Ser Ala Asp Tyr Gly Asp Ile Ile Phe Asp  
195 200 205

Gly Asn Leu Lys Arg Thr Ala Lys Glu Asn Ala Ala Asp Val Asn Gly  
210 215 220

Val Thr Val Ser Ser Gln Ala Ile Ser Met Gly Ser Gly Gly Lys Ile  
225 230 235 240

Thr Thr Leu Arg Ala Lys Ala Gly His Gln Ile Leu Phe Asn Asp Pro  
245 250 255

Ile Glu Met Ala Asn Gly Asn Asn Gln Pro Ala Gln Ser Ser Lys Leu  
260 265 270

Leu Lys Ile Asn Asp Gly Glu Gly Tyr Thr Gly Asp Ile Val Phe Ala  
275 280 285

Asn Gly Ser Ser Thr Leu Tyr Gln Asn Val Thr Ile Glu Gln Gly Arg  
290 295 300

Ile Val Leu Arg Glu Lys Ala Lys Leu Ser Val Asn Ser Leu Ser Gln  
305 310 315 320

Thr Gly Gly Ser Leu Tyr Met Glu Ala Gly Ser Thr Trp Asp Phe Val  
325 330 335

Thr Pro Gln Pro Pro Gln Gln Pro Pro Ala Ala Asn Gln Leu Ile Thr  
340 345 350

Leu Ser Asn Leu His Leu Ser Leu Ser Ser Leu Leu Ala Asn Asn Ala  
355 360 365

Val Thr Asn Pro Pro Thr Asn Pro Pro Ala Gln Asp Ser His Pro Ala  
370 375 380

Val Ile Gly Ser Thr Thr Ala Gly Ser Val Thr Ile Ser Gly Pro Ile  
385 390 395 400

Phe Phe Glu Asp Leu Asp Asp Thr Ala Tyr Asp Arg Tyr Asp Trp Leu  
405 410 415

Gly Ser Asn Gln Lys Ile Asn Val Leu Lys Leu Gln Leu Gly Thr Lys

420

425

430

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Lys Tyr Gly Tyr Gln Gly Ser Trp Lys Leu  
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Arg Ser Ala His Ser Ala Ile Gln Ala Ser Val Asp Gly Arg Ser Tyr  
 35 40 45

Cys Arg Gly Leu Trp Val Ser Gly Val Ser Asn Phe Phe Tyr His Asp  
 50 55 60

Arg Asp Ala Leu Gly Gln Gly Tyr Arg Tyr Ile Ser Gly Gly Tyr Ser  
 65 70 75 80

Leu Gly Ala Asn Ser Tyr Phe Gly Ser Ser Met Phe Gly Leu Ala Phe  
 85 90 95

Thr Glu Val Phe Gly Arg Ser Lys Asp Tyr Val Val Cys Arg Ser Asn  
 100 105 110

His His Ala Cys Ile Gly Ser Val Tyr Leu Ser Thr Gln Gln Ala Leu  
 115 120 125

Cys Gly Ser Tyr Leu Phe Gly Asp Ala Phe Ile Arg Ala Ser Tyr Gly  
 130 135 140

Phe Gly Asn Gln His Met Lys Thr Ser Tyr Thr Phe Ala Glu Glu Ser  
 145 150 155 160

Asp Val Arg Trp Asp Asn Asn Cys Leu Ala Gly Glu Ile Gly Ala Gly  
 165 170 175

Leu Pro Ile Val Ile Thr Pro Ser Lys Leu Tyr Leu Asn Glu Leu Arg  
180 185 190

Pro Phe Val Gln Ala Glu Phe Ser Tyr Ala Asp His Glu Ser Phe Thr  
195 200 205

Glu Glu Gly Asp Gln Ala Arg Ala Phe Lys Ser Gly His Leu Leu Asn  
210 215 220

Leu Ser Val Pro Val Gly Val Lys Phe Asp Arg Cys Ser Ser Thr His  
225 230 235 240

Pro Asn Lys Tyr Ser Phe Met Ala Ala Tyr Ile Cys Asp Ala Tyr Arg  
245 250 255

Thr Ile Ser Gly Thr Glu Thr Thr Leu Leu Ser His Gln Glu Thr Trp  
260 265 270

Thr Thr Asp Ala Phe His Leu Ala Arg His Gly Val Val Val Arg Gly  
275 280 285

Ser Met Tyr Ala Ser Leu Thr Ser Asn Ile Glu Val Tyr Gly His Gly  
290 295 300

Arg Tyr Glu Tyr Arg Asp Ala Ser Arg Gly Tyr Gly Leu Ser Ala Gly  
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Ser Arg Val Arg Phe  
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